

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 8, 2002, 09:30:40 ; Search time 25.41 Seconds

(Without alignments) 211.767 Million cell updates/sec

Title: US-09-640-211A-2347

Sequence: 1 PDVRRGNITTEEDLLIMELHSHKNGNRSKIAKHLPGRTONEIKNFWRTRIQKHIKO 56

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	298	97.1	217	2	T06455 Myb26 protein - ga
2	287.5	93.6	198	1	JQ0959 myb-related protei
3	281	91.5	205	1	JQ0958 myb-related protei
4	279	90.9	333	2	T09736 myb-related protei
5	279	90.9	333	2	T09735 ABA-induced myb-re
6	279	90.9	333	2	T09737 dehydration-induce
7	259	84.4	286	2	H96706 myb-relate
8	259	84.4	293	2	T09758 myb-relate
9	255	83.1	216	2	D96520 myb-related prote
10	254	82.7	278	2	C86383 hypothetical prote
11	246	80.1	273	1	JQ2330 Probable Myb-like
12	225	73.3	141	2	T51642 Myb transcription
13	217	70.7	261	2	T06650 Probable transcrip
14	215	70.0	234	2	T51666 myb-related protei
15	215	70.0	256	2	T49254 myb DNA binding pr
16	210	68.4	218	2	T51681 myb-related transcr
17	205	66.8	118	2	T51684 myb-related transcr
18	203	66.1	204	2	T51659 myb-related transcr
19	196	63.8	274	2	T07393 myb-related transcr
20	195	63.5	327	2	T01038 myb-related protei
21	195	63.5	331	1	S69190 myb-related protei
22	194	63.2	238	2	T46166 MYB27 protein - Ar
23	194	63.2	268	1	JQ0951 myb-related protei
24	194	63.2	378	2	T51647 myb-related transcr
25	192	62.5	414	2	A86229 hypothetical prote
26	190	61.9	217	2	T51671 myb-related transcr
27	190	61.9	282	2	C96687 hypothetical prote
28	190	61.9	376	2	T03988 Myb-like transcrip
29	190	61.9	399	1	A39697 maize myb-related

30	190	61.9	553	2	T03762 myb-related transcr
31	189	61.6	203	2	T51653 myb-related transcr
32	189	61.6	263	2	T48607 Probable transcrip
33	189	61.6	370	2	C96664 hypothetical protei
34	189	61.6	553	2	T06179 myb-related protei
35	188	61.2	265	2	T07395 myb-related transcr
36	188	61.2	280	1	S26604 myb-related protei
37	188	61.2	325	2	T53509 Probable transcrip
38	188	61.2	421	1	S24244 myb-related protei
39	188	61.2	745	2	A71448 Probable MYB trans
40	187	60.9	274	2	D86300 hypothetical prote
41	187	60.9	278	2	T03850 myb-related protei
42	186	60.6	279	2	T03830 Probable myb facto
43	186	60.6	1297	2	T52065 Probable myb-relat
44	185	60.3	369	2	T01196 transcription fact
45	185	60.3	371	2	T00438 Probable MYB famil

ALIGNMENTS

RESULT 1
T06455
Myb26 protein - garden pea
C:Species: Pisum sativum (garden pea)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000
C:Accession: T06455
R:Umarl, A.; Strommer, J.
Plant J. 12, 1273-1284, 1997
A>Title: Myb26: A MYB-like protein of pea flowers with affinity for promoters of phen
A:Reference number: Z15690; MIMD:98112025
A:Accession: T06455
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-217 <1IM>
A:Cross-references: EMBL:Y11105; NID:q1841474; PIDN:CAAT1997.1; PID:q1841475
C:Superfamily: Arabidopsis myb-related protein 2; myb DNA-binding repeat homology
C:Keywords: DNA binding
F:11-63/Domain: myb DNA-binding repeat homology <MYB>
F:64-113/Domain: myb DNA-binding repeat homology <MYB1>

Query Match 97.1%; Score 298; DB 2; Length 217;
Best Local Similarity 96.4%; Pred. No. 1.3e-28;
Matches 54; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 PDVRRGNITTEEDLLIMELHSHKNGNRSKIAKHLPGRTONEIKNFWRTRIQKHIKO 56
DB 65 PDVRRGNITTEEDLLIMELHSHKNGNRSKIAKHLPGRTONEIKNFWRTRIQKHIKO 120

RESULT 2
JQ0959
myb-related protein 340 - garden snapdragon
C:Species: Antirrhinum majus (garden snapdragon)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 02-Sep-1997
C:Accession: JQ0959
R:Jackson, D.; Cullane-Macra, F.; Prescott, A.G.; Roberts, K.; Martin, C.
Plant Cell 3, 115-125, 1991
A>Title: Expression patterns of myb genes from Antirrhinum flowers.
A:Reference number: JQ0956; MIMD:93005689
A:Accession: JQ0959
A:Molecule type: mRNA
A:Residues: 1-198 <JAC>
A:Experimental source: strain JI-522
C:Comment: This protein is specifically expressed in flowers.
C:Superfamily: Arabidopsis myb-related protein 2; myb DNA-binding repeat homology
C:Keywords: DNA binding; duplication
F:10-62/Domain: myb DNA-binding repeat homology <MYB1>
F:63-113/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 93.6%; Score 287.5; DB 1; Length 198;

Best Local Similarity 94.7%; Pred. No. 2,1e-27;
Matches 54; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 1 PDVRCNITTEEOQLIMELHAKMGNRMSKIAKHLPGRTDNEIKNFWRTRIQKHQ 56
|||||
Db 64 PDVRCNITTEEOQLIMELHAKMGNRMSKIAKHLPGRTDNEIKNFWRTRIQKHQ 120

RESULT 3
J00958

myb-related protein 305 - garden snapdragon

C:Species: Antirrhinum majus (garden snapdragon)

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 24-Jul-1997

C:Accession: J00958

R:Jackson, D.; Culianez-Macia, F.; Prescott, A.G.; Roberts, K.; Martin, C.

A:Title: Expression patterns of myb genes from Antirrhinum flowers.

A:Reference number: J00956; MUID:93005689

A:Accession: J00958

A:Molecule type: mRNA

A:Residues: 1-205 <ITU>

A:Experimental source: strain J1:522

C:Comment: This protein is specifically expressed in flowers.

C:Superfamily: Arabidopsis myb-related protein 2; myb DNA-binding repeat homology

F:10-62/Domain: myb DNA-binding repeat homology <MYB1>

F:63-113/Domain: myb DNA-binding repeat homology <MYB2>

Query Match 91.5%; Score 281; DB 1; Length 205;
Best Local Similarity 91.1%; Pred. No. 1.4e-26;

Matches 51; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PDVRCNITTEEOQLIMELHAKMGNRMSKIAKHLPGRTDNEIKNFWRTRIQKHQ 56
|||||
Db 64 PDVRCNITTEEOQLIMELHAKMGNRMSKIAKHLPGRTDNEIKNFWRTRIQKHQ 119

RESULT 4
T09736

myb-related protein Cpm5 - Craterostigma plantagineum

C:Species: Craterostigma plantagineum

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T09736

R:Turriaga, G.; Leyns, L.; Villegas, A.; Charalbeh, R.; Salamini, F.; Bartels, D.

A:Title: A family of novel myb-related genes from the resurrection plant Craterostigma

A:Reference number: Z16838; MUID:97134962

A:Accession: T09736

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-333 <ITU>

A:Cross-references: EMBL:U03916; NID:g1002797; PIDN:AAB58313.1; PID:g1002798

C:Genetics:

A:Gene: cpm5

A:Introns: 60/1; 103/2

C:Superfamily: unassigned myb DNA-binding repeat proteins; myb DNA-binding repeat homology

C:Keywords: DNA binding; transcription factor; transcription regulation

F:77-126/Domain: myb DNA-binding repeat homology <MYB>

Query Match 90.9%; Score 279; DB 2; Length 333;
Best Local Similarity 85.7%; Pred. No. 4e-26;
Matches 48; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PDVRCNITTEEOQLIMELHAKMGNRMSKIAKHLPGRTDNEIKNFWRTRIQKHQ 56
|||||
Db 78 PDVRCNITTEEOQLIMELHAKMGNRMSKIAKHLPGRTDNEIKNFWRTRIQKHQ 133

RESULT 5
T09735

ABA-induced myb-related protein Cpm10 - Craterostigma plantagineum

C:Species: Craterostigma plantagineum

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T09735

R:Turriaga, G.; Leyns, L.; Villegas, A.; Charalbeh, R.; Salamini, F.; Bartels, D.

A:Title: A family of novel myb-related genes from the resurrection plant Craterostigma

A:Reference number: Z16838; MUID:97134962

A:Accession: T09735

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-333 <ITU>

A:Cross-references: EMBL:U03915; NID:g1002795; PIDN:AAC13876.1; PID:g1002796

C:Genetics:

A:Gene: cpm10

A:Introns: 60/1; 103/2

C:Superfamily: unassigned myb DNA-binding repeat proteins; myb DNA-binding repeat homology

F:77-126/Domain: myb DNA-binding repeat homology <MYB>

Query Match 90.9%; Score 279; DB 2; Length 333;
Best Local Similarity 85.7%; Pred. No. 4e-26;

Matches 48; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PDVRCNITTEEOQLIMELHAKMGNRMSKIAKHLPGRTDNEIKNFWRTRIQKHQ 56
|||||
Db 78 PDVRCNITTEEOQLIMELHAKMGNRMSKIAKHLPGRTDNEIKNFWRTRIQKHQ 133

RESULT 6
T09737

dehydration-induced myb-related protein Cpm7 - Craterostigma plantagineum

C:Species: Craterostigma plantagineum

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T09737

R:Turriaga, G.; Leyns, L.; Villegas, A.; Charalbeh, R.; Salamini, F.; Bartels, D.

A:Title: A family of novel myb-related genes from the resurrection plant Craterostigma

A:Reference number: Z16838; MUID:97134962

A:Accession: T09737

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-335 <ITU>

A:Cross-references: EMBL:U03917; NID:g1002799; PIDN:AAB58314.1; PID:g1002800

C:Genetics:

A:Gene: cpm7

C:Superfamily: unassigned myb DNA-binding repeat proteins; myb DNA-binding repeat homology

C:Keywords: DNA binding; transcription factor; transcription regulation

F:76-125/Domain: myb DNA-binding repeat homology <MYB>

Query Match 90.9%; Score 279; DB 2; Length 335;
Best Local Similarity 85.7%; Pred. No. 4.1e-26;
Matches 48; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PDVRCNITTEEOQLIMELHAKMGNRMSKIAKHLPGRTDNEIKNFWRTRIQKHQ 56
|||||
Db 77 PDVRCNITTEEOQLIMELHAKMGNRMSKIAKHLPGRTDNEIKNFWRTRIQKHQ 132

RESULT 7
H96706

probable transcription factor T22E19.5 (imported) - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: H96706

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, A.; Hughes, B.; Hulzart, L.

A:Title: Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, A.; Hughes, B.; Hulzart, L.

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.; Liu, Y.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Malt, R.; Marzla, R.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: H96706

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-286 <STO>

A:Cross-references: GB:AE005173; NID:g6715735; PIDN:AAF26496.1; GSPDB:GN00141

C:Genetics:

A:Gene: T22E19.5

A:Map position: 1

C:Superfamily: maize myb-related protein 1; myb DNA-binding repeat homology

Query Match

Best Local Similarity 84.4%; Score 259; DB 2; Length 286;
Matches 43; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PDVRRGNITTEEDLLIMELHAKGNRMSKIAKHLPGRTDNEIKNFWRTRIOKHIO 56

Db 70 PDIRGNLTPEQDLILHLSKMGNRMSKIAQYLPGRDNEIKNYWTRVQKQAKO 125

RESULT 8

myb-related protein - upland cotton

N:Alternate names: MYB-like DNA-binding domain protein

C:Species: Gossypium hirsutum (upland cotton)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-Aug-1999

C:Accession: T09758

R:Loguercio, L.L.; Zhang, J.; Wilkins, T.A.

submitted to the EMBL Data Library, November 1997

A:Description: Structure and expression of six classes of myb-domain genes in allotetrap

A:Reference number: Z16842

A:Accession: T09758

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-293 <LOG>

A:Cross-references: EMBL:AF034133; NID:g2921337; PID:g2921338

A:Experimental source: cultivar Acala 5J-2; ovule

C:Genetics:

A:Note: CmY-N

C:Superfamily: Arabidopsis myb-related protein 2; myb DNA-binding repeat homology

C:Keywords: DNA binding; transcription regulation

F:70-119/Domain: myb DNA-binding repeat homology <MYB>

Query Match

Best Local Similarity 84.4%; Score 259; DB 2; Length 293;
Matches 43; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PDVRRGNITTEEDLLIMELHAKGNRMSKIAKHLPGRTDNEIKNFWRTRIOKHIO 56

Db 71 PEIKRGNITTEEDLLILHLSKMGNRMSKIAQYLPGRDNEIKNYWTRVQKQAKO 126

RESULT 9

hypothetical protein T2J15.9 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: D96520

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: D96520

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-216 <STO>

A:Cross-references: GB:AE005173; NID:g10645470; PIDN:AMG21584.1; GSPDB:GN00141

C:Genetics:

A:Gene: T2J15.9

A:Map position: 1

C:Superfamily: trichome differentiation protein GL1; myb DNA-binding repeat homology

Query Match

Best Local Similarity 83.1%; Score 255; DB 2; Length 216;
Matches 41; Conservative 11; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PDVRRGNITTEEDLLIMELHAKGNRMSKIAKHLPGRTDNEIKNFWRTRIOKHIO 55

Db 56 PDIRBGDISIQEQFIILHLSKMGNRMSKIAQYLPGRDNEIKNYWTRVQKQAK 110

RESULT 10

probable Myb-like protein (Myb26) [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: C86383

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

ansen, N.F.; Hughes, B.; Hutzar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719

A:Accession: C86383

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-278 <STO>

A:Cross-references: GB:AE005172; NID:g11067290; PIDN:AAQ28818.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

C:Superfamily: anthocyanin biosynthesis regulatory protein; myb DNA-binding repeat ho

Query Match

Best Local Similarity 82.7%; Score 254; DB 2; Length 278;
Matches 41; Conservative 12; Mismatches 3; Indels 0; Gaps 0;

Qy 1 PDVRRGNITTEEDLLIMELHAKGNRMSKIAKHLPGRTDNEIKNFWRTRIOKHIO 56

Db 64 PDIRGNLTPEQDLILHLSKMGNRMSKIAQYLPGRDNEIKNYWTRVQKQAKO 119

RESULT 11

MYB transcription factor (Atmyb2) [imported] - Arabidopsis thaliana

N:Alternate names: myb-related protein 2; AtMYB2 protein

C:Species: Arabidopsis thaliana (mouse-ear cross)

C>Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 23-Mar-2001

C:Accession: J02390; B84912

R:Urao, T.; Yamaguchi-Shinozaki, K.; Urao, S.; Shinozaki, K.

Plant Cell 5, 1529-1539, 1993

A:Title: An arabidopsis myb homolog is induced by dehydration stress and its gene pro

A:Reference number: J02390; MUID:94146551

A:Accession: J02390

A:Molecule type: mRNA

A:Residues: 1-273 <STO>

A:Cross-references: DDBJ:D14712; NID:g455462; PIDN:BA00534.1; PID:g506189

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentley, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,

euss,D.: Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, A.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A:Reference number: A84420; MUID:20083487
 A:Accession: B84912
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-273 <STO>
 A:Cross-references: GB:AE002093; NID:92275197; PIND:AA63819.1; GSPDH:GN00139
 C:Comment: The expression of the gene encoding for this protein is induced by dehydration
 C:Genetics:
 A:Gene: Atmyb2; AC2947190
 A:Map position: 2
 A:Introns: 53/1; 96/2
 C:Superfamily: Arabidopsis myb-related protein 2; myb DNA-binding repeat homology
 C:Keywords: DNA binding; duplication
 E:17-69/Domain: myb DNA-binding repeat homology <MYB1>
 E:70-120/Domain: myb DNA-binding repeat homology <MYB2>

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Query Match          80.1%; Score 246; DB 1; Length 273;
Best Local Similarity 76.4%; Pred. No. 3.2e-22;
Matches 42; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

OY      1 PDVRRGNTTEEQLLIMELHAKGNRMSKIAKHLPGRTDNEKNPWRRIQKHK 55
          |||||  ||| :|||: |||||:|||||:|||||:|||||:|
Db      71 PDVRRGNTTLEQFMTLKHSLMGKRSKIAQYLPGRDNEIKNWRIVQKQAK 125

RESULT  12

T51642
Probable transcription factor MYB21 [imported] - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
C:Accession: T51642
R:Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.; J
; Paz-Ares, J.; Weissbach, B.
Plant J. 16, 263-276, 1998
A>Title: Towards functional characterisation of the members of the R2R3-MYB gene from Ar
A:Reference number: Z14349; MUID:9839469
A:Accession: T51642
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-141 <KRA>
A:Cross-references: EMBL:AF062870; PIDN:AAC83592.1
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: MYB21
C:Superfamily: Arabidopsis myb-related protein 2; myb DNA-binding repeat homology

```

```

Query Match      73.3% Score 225; DB 2; Length 141;
Best Local Similarity 97.6% Pred. No. 5.4e-20;
Matches 40; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      16 IMELHAKGCMNRMSKIAKHLPGRTDNEIKNFWRTRIQKHQ 56
          |||
Db       1 IMELHAKGCMNRMSKIAKHLPGRTDNEIKNFWRTRIQKHQ 41

RESULT  13

T06650
myb-related protein homolog T6G15.30 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 19-May-2000
C:Accession: T06650
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15791
A:Accession: T06650
A:Molecule type: DNA
A:Residues: 1-261 <BEV>

```

A:Cross-references: EMBL:AL049656; GSPDB:GN00065; ATSP:TP615...30
A:Experimental source: cultivar Columbia; BAC clone T615
C:Genetics:
A:Gene: ATSP:T6G15.30
A:Map position: 4
A:Introns: 39/1; 82/2
C:Superfamily: unassigned myb DNA-binding repeat proteins; myb DNA-binding hom
P:56-106/Domain: myb DNA-binding repeat homology <MYB>

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Query Match 70.7%; Score 217; DB 2; Length 261;
Best Local Similarity 67.3%; Pred. No. 9.9e-19;
Matches 37; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

OY 1 PDVRCNTTTEBQLIMELHAKWGNRSKIAKHLPGRTDNETIKNWRTRIQKHK 55
||:||||| ||: ||:||||||||||| ||: ||||||||||| ||: |||
Db 57 PDLKKGQITTPHESITLHAKWGNRMTIARSLPGRTDNETIKNWRTRHFFKKKK 111

RESULT 14
T51666
myb-related transcription factor MYB59 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_rev1sion 18-Aug-2000 #text_change 31-Mar-2001
C:Accession: T51666
R:Kranz, H.D.; Denekamp, M.; Greco, R.; Jin, H.; Kranz, H.D.; Denekamp, M.; Greco, R.;
Paz-Ares, J.; Weisshart, B.
Plant J. 16, 263-276, 1998
A>Title: Towards functional characterisation of the members of the R2R3-MYB gene from
A:Reference number: 214349; MUID:9839469
A:Accession: T51666
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-234 <KRA>
A:Cross-references: EMBL:AF062894; PIDN:AAC83616.1
A:Experimental source: cultivar Columbia
C:Genetics:
A:Gene: MYB59
C:Superfamily: Antirrhinum myb-related protein 315; myb DNA-binding repeat homology
C:Keywords: transcription factor

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RESULT 15

749254
MYB DNA binding protein-like - Arabidopsis thaliana

N:Alternate names: protein.F12M12.100

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000

C:Accession: T49254

R:Jordan, N.; Banerji, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S

Submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25020

A:Accession: T49254

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-256 <J08>

A:Cross-references: EMBL:AL355775; GSPDB:GN00061; ATSP:F12M12.100

A:Experimental source: cultivar Columbia; BAC clone F12M12

C:Genetics:

A:Gene: ATSP:F12M12.100

A:Map position: 3

A:Introns: 40/1; 83/2

C:Superfamily: Antirrhinum myb-DNA-related protein 315; myb DNA-binding repeat homology


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Db      1 MDKPPDSCSDVEVRKGPMTMEDLLILINYIANHGEVSNLSAKAAGLKRGTGKSCRL 57
QY      61 RWLNYLR 67
        |||||
Db      58 RWLNYLR 64

RESULT  2
P81391
ID      P81391      PRELIMINARY:      PRT:      205 AA.
AC      P81391:
DT      01-JUN-1998 (TREMBLrel. 06, Created)
DE      01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      MYB-RELATED PROTEIN 305.
GN      MYB 305.
OS      Antirrhinum majus (Garden snapdragon).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC      Asteridae; euasterids I; Linales; Veroniceae; Antirrhinum.
OX      NCBI_TaxID=4151;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=J1:522; TISSUE=FLOWER BUDS;
RX      MEDLINE=93005689; PubMed=1840903;
RA      Jackson D., Cuatrecasas-Macia F., Prescott A.G., Roberts K., Martin C.,
RT      "Expression patterns of myb genes from Antirrhinum flowers."
RT      Plant Cell 3:115-125(1991).
CC      -1- FUNCTION: MAY BE A TRANSCRIPTIONAL ACTIVATOR.
CC      -1- TISSUE SPECIFICITY: MATURE FLOWER.
CC      -1- DEVELOPMENTAL STAGE: FIRST DETECTED IN 15-20 MM BUDS.
CC      -1- SIMILARITY: BELONGS TO THE MYB FAMILY OF PROTEINS.
DR      HSP: P01103; IPOM.
DR      TRANSFAC: T02907; -.
DR      InterPro: IPR001395; Aldo_ket_red.
DR      InterPro: IPR001005; Myb_DNA_bind.
DR      Pfam: PF00249; myb_DNA-binding; 2.
DR      SMART: SM00395; SANT; 2.
DR      PROSITE: PS00063; ALDO_KETO_REDUCTASE_3; UNKNOWN_1.
DR      PROSITE: PS00037; MYB_1; UNKNOWN_1.
DR      PROSITE: PS00334; MYB_2; 1.
DR      PROSITE: PS00900; MYB_3; 2.
KW      Nuclear protein; DNA-binding; Repeat; Transcription regulation.
FT      DNA_BIND 10 62 MYB.
FT      DNA_BIND 63 103 MYB.
SQ      SEQUENCE 205 AA; 23507 MW; A0B131BA7C309CB CRC64;

Query Match      83.7%; Score 304; DB 10; Length 205;
Best Local Similarity 86.6%; Pred. No. 8.4e-30;
Matches 58; Conservative 3; Mismatches 2; Indels 4; Gaps 1;

QY      1 MDKPPDSCSDVEVRKGPMTMEDLLILINYIANHGEVSNLSAKAAGLKRGTGKSCRL 60
        |||||
        |||||
Db      1 MDKPPCN----SDVEVRKGPMTMEDLLILINYIANHGEVSNLSAKAAGLKRGTGKSCRL 56

QY      61 RWLNYLR 67
        |||||
Db      57 RWLNYLR 63

RESULT  3
O9SPG9
ID      O9SPG9      PRELIMINARY:      PRT:      214 AA.
AC      O9SPG9:
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      PUTATIVE TRANSCRIPTION FACTOR.
GN      MYB24.
OS      Arabidopsis thaliana (Mouse-ear cress).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC      eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX      NCBI_TaxID=3702;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CV. COLUMBIA;
RX      MEDLINE=99056848; PubMed=9839469;
RA      Kranz H.D., Denekamp M., Greco R., Jin H., Leyva A., Weissner R.C.,
RA      Petroni K., Urzainqui A., Bevan M., Martin C., Smeekens S.,
RA      Tonelli C., Paz-Ares J., Weisshaar B.;
RT      "Towards functional characterisation of the members of the R2R3-MYB
RT      gene family from Arabidopsis thaliana."
RT      Plant J. 16:263-276(1998).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CV. COLUMBIA;
RA      Stracke R., Weisshaar B.;
RT      "R2R3-MYB transcription factor gene nomenclature in Arabidopsis
RT      thaliana."
RT      Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=COLUMBIA;
RX      MEDLINE=98069011; PubMed=9405937;
RA      Kotani H., Nakamura Y., Sato S., Kaneko T., Asamizu E., Miyajima N.,
RA      Tabata S.;
RT      "Structural analysis of Arabidopsis thaliana chromosome 5. II.
RT      Sequence features of the regions of 1,044,062 bp covered by thirteen
RT      physically assigned P1 clones."
RL      DNA Res. 4:291-300(1997).
DR      EMBL: AF175987; AAD53092.1; -.
DR      EMBL: AB006702; BAB11590.1; -.
DR      HSP: P01103; IPOM.
DR      InterPro: IPR001395; Aldo_ket_red.
DR      InterPro: IPR001005; Myb_DNA_bind.
DR      Pfam: PF00249; myb_DNA-binding; 2.
DR      SMART: SM00395; SANT; 2.
DR      PROSITE: PS00063; ALDO_KETO_REDUCTASE_3; UNKNOWN_1.
DR      PROSITE: PS00037; MYB_1; UNKNOWN_1.
DR      PROSITE: PS00334; MYB_2; 1.
DR      PROSITE: PS00900; MYB_3; 2.
SQ      SEQUENCE 214 AA; 24459 MW; BSDAE2471F75673F CRC64;

Query Match      80.4%; Score 292; DB 10; Length 214;
Best Local Similarity 80.6%; Pred. No. 2.7e-28;
Matches 54; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY      1 MDKPPDSCSDVEVRKGPMTMEDLLILINYIANHGEVSNLSAKAAGLKRGTGKSCRL 60
        |||||
        |||||
Db      1 MEKRESSGSGSDAEVRKGPMTMEDLLILINYIANHGEVSNLSAKAAGLKRGTGKSCRL 60

QY      61 RWLNYLR 67
        |||||
Db      61 RWLNYLR 67

RESULT  4
O9AVB7
ID      O9AVB7      PRELIMINARY:      PRT:      184 AA.
AC      O9AVB7:
DT      01-JUN-2001 (TREMBLrel. 17, Created)
DT      01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      LHMV PROTEIN.
GN      LHMV.
OS      Lilium hybrid division I.
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Lillales; Liliaceae; Lilium.
OX      NCBI_TaxID=156532;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CV. MONTREUX; TISSUE=TEPAL;

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RA Nakatsuka A., Izumi Y., Yamagishi M.;
RT "Isolation and characterization of the genes related to anthocyanin
biosynthesis in Asiatic hybrid lily.";
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB058642; BAB40790.1; -.
DR HSSP: P01103; IPOM.
DR InterPro: IPR001395; Aldo_ket_red.
DR InterPro: IPR001005; MYB_DNA_bind.
DR Pfam: PF00249; MYB_DNA-binding; 2.
DR SMART: SM00395; SANT; 2.
DR PROSITE: PS00063; ALDO_KETO_REDUCTASE_3; UNKNOWN_1.
DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
DR PROSITE: PS00034; MYB_2; 1.
DR PROSITE: PS00090; MYB_3; 2.
SO SEQUENCE 184 AA; 21222 MW; 44C2993527191EDD CRC64;

Query Match 79.1%; Score 287; DB 10; Length 184;
Best Local Similarity 79.1%; Pred. No. 9, 5e-28;
Matches 53; Conservative 7; Mismatches 3; Indels 4; Gaps 1;

OY 1 MDKRPDDSGKSODVEVRKGPMTMEDLLINIANHSGSNLSAKAGLKRKSCRL 60
DB 1 MDKRPDDSGKSODVEVRKGPMTMEDLLINIANHSGSNLSAKAGLKRKSCRL 56
OY 61 RWLNLYR 67
DB 57 RWLNLYR 63

RESULT 5
P81396 PRELIMINARY; PRT; 198 AA.
AC P81396;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYB-RELATED PROTEIN 340.
GN MYB 340.
OS Antirrhinum majus (Garden snapdragon).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
OX NCBI_TaxID=4151;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J1:522; TISSUE=FLOWER BUDS;
RX MEDLINE=93005689; PubMed=1840903;
RA Jackson D., Culianez-Macia F., Prescott A.G., Roberts K., Martin C.;
RT "Expression patterns of myb genes from Antirrhinum flowers.";
RL Plant Cell 3:115-125(1991).
CC -1- FUNCTION: MAY BE A TRANSCRIPTIONAL ACTIVATOR.
CC -1- TISSUE SPECIFICITY: MATURE FLOWER.
CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED IN 0-5 MM BUDS.
CC -1- SIMILARITY: BELONGS TO THE MYB FAMILY OF PROTEINS.
DR HSSP: J00959; J00959.
DR HSSP: P01103; IPOM.
DR TRANSFAC: T02929; -.
DR InterPro: IPR001395; Aldo_ket_red.
DR InterPro: IPR001005; MYB_DNA_bind.
DR Pfam: PF00249; MYB_DNA-binding; 2.
DR SMART: SM00395; SANT; 2.
DR PROSITE: PS00063; ALDO_KETO_REDUCTASE_3; UNKNOWN_1.
DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
DR PROSITE: PS00090; MYB_3; 2.
KM Nuclear protein; DNA-binding; Repeat; Transcription regulation.
FT DNA_BIND 10 62 MYB.
FT DNA_BIND 63 103 MYB.
SO SEQUENCE 198 AA; 22846 MW; 5897CE3787BC6575 CRC64;

Query Match 79.1%; Score 287; DB 10; Length 198;
Best Local Similarity 79.1%; Pred. No. 1e-27;

Matches 53; Conservative 7; Mismatches 3; Indels 4; Gaps 1;

OY 1 MDKRPDDSGKSODVEVRKGPMTMEDLLINIANHSGSNLSAKAGLKRKSCRL 60
DB 1 MDKRPDDSGKSODVEVRKGPMTMEDLLINIANHSGSNLSAKAGLKRKSCRL 56
OY 61 RWLNLYR 67
DB 57 RWLNLYR 63

RESULT 6
O22684 PRELIMINARY; PRT; 226 AA.
AC O22684;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ATMYB3.
GN ATMYB3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Noji M., Urao T., Shinozaki K.Y., Shinozaki K.;
RT "Molecular cloning of two cDNAs encoding novel myb homologs from
Arabidopsis (Accession Nos. AB005888 and AB005889) (GGR98-111).";
RL Plant Physiol. 117:720-720(1998).
DR EMBL: AB005888; BAA21618.1; -.
DR HSSP: P01103; IPOM.
DR InterPro: IPR001395; Aldo_ket_red.
DR InterPro: IPR001005; MYB_DNA_bind.
DR Pfam: PF00249; MYB_DNA-binding; 2.
DR SMART: SM00395; SANT; 2.
DR PROSITE: PS00063; ALDO_KETO_REDUCTASE_3; UNKNOWN_1.
DR PROSITE: PS00037; MYB_1; UNKNOWN_1.
DR PROSITE: PS00090; MYB_3; 2.
SO SEQUENCE 226 AA; 25268 MW; CF22A28650AB898D CRC64;

Query Match 78.8%; Score 286; DB 10; Length 226;
Best Local Similarity 88.1%; Pred. No. 1.6e-27;
Matches 52; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 9 SGRSDVEVRKGPMTMEDLLINIANHSGSNLSAKAGLKRKSCRLRWLNLYR 67
DB 12 SGRSDVEVRKGPMTMEDLLINIANHSGSNLSAKAGLKRKSCRLRWLNLYR 70
OY 61 RWLNLYR 67
DB 57 RWLNLYR 63

RESULT 7
O91K95 PRELIMINARY; PRT; 226 AA.
AC O91K95;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ATMYB3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneo T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RT Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN=COLUMBIA;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety p1,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AF000371; BAB02527.1; -.
DR EMBL; AB018114; BAB02527.1; JOINED.
DR HSSP; P01103; IPOW.
DR InterPro: IPR001005; Myb_DNA_bind.
DR Pfam; PF00249; myb_DNA-binding; 2.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS00063; ALDOLETO_REDUCTASE_3; UNKNOWN_1.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
SQ SEQUENCE 226 AA; 25351 MW; D29479EBFDID59CC CRC64;

Query Match 78.8%; Score 286; DB 10; Length 226;
Best Local Similarity 88.1%; Pred. No. 1.6e-27;
Matches 52; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 9 SGKSQDVEVRKGPWTMEDLILYINAHGSGSNLSAKAAGLRKRGKSCRLRWLNTLR 67
DB 12 SGSSAEAEVRKGPWTMEDLILYINAHGSGSNLSAKAAGLRKRGKSCRLRWLNTLR 70

RESULT 8
Q9SSA1 PRELIMINARY; PRT; 206 AA.
AC Q9SSA1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE POTATIVE TRANSCRIPTION FACTOR.
GN FAP13.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
RA Ranning C.M., Koo H., Fujii C.Y., Ulterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC F4P13 genomic sequence.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC009325; AAF01538.1; -.
DR HSSP; P01103; IPOW.
DR InterPro: IPR001005; Myb_DNA_bind.
DR Pfam; PF00249; myb_DNA-binding; 2.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
SQ SEQUENCE 206 AA; 23717 MW; 61DC2A28674D87F7 CRC64;

Query Match 71.6%; Score 260; DB 10; Length 206;
Best Local Similarity 79.7%; Pred. No. 2.5e-24;
Matches 47; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 9 SGKSQDVEVRKGPWTMEDLILYINAHGSGSNLSAKAAGLRKRGKSCRLRWLNTLR 67
DB 17 SQKEBEGTVRKGPWTMEDLILYINAHGSGSNLSAKAAGLRKRGKSCRLRWLNTLR 75

RESULT 9

Q39552
ID Q39552 PRELIMINARY; PRT; 335 AA.
AC Q39552;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CPM7.
GN CPM7.
OS Craterostigma plantagineum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids I; Lamiales; Lamiales incertae sedis; Toreniaeae;
OC Craterostigma.
OX NCBI_TaxID=4153;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97134962; PubMed=8980522;
RA Iturriaga G., Leyns L., Villegas A., Charalbeh R., Salami F.,
RA Bartels D.;
RT "A family of novel myb-related genes from the resurrection plant
RT Craterostigma plantagineum are specifically expressed in callus and
RT roots in response to ABA or desiccation.";
RL Plant Mol. Biol. 32:707-716(1996).
DR EMBL; U33917; AAB58314.1; -.
DR HSSP; P01103; IPOW.
DR TRANSFAC; T02881; -.
DR InterPro: IPR001005; Myb_DNA_bind.
DR Pfam; PF00249; myb_DNA-binding; 2.
DR SMART; SM00395; SANT; 2.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00334; MYB_2; 1.
DR PROSITE; PS50090; MYB_3; 2.
SQ SEQUENCE 335 AA; 38258 MW; 85537EB4F52A6AA3 CRC64;

Query Match 69.0%; Score 250.5; DB 10; Length 335;
Best Local Similarity 67.2%; Pred. No. 6.7e-23;
Matches 45; Conservative 10; Mismatches 7; Indels 5; Gaps 1;

OY 1 MDKKPDGSGKSQDVEVRKGPWTMEDLILYINAHGSGSNLSAKAAGLRKRGKSCRL 60
DB 15 INEDDDDS-----DLRGPWTVEDLILYINAHGSGSNLSAKAAGLRKRGKSCRL 69

OY 61 RMLNTLR 67
DB 70 RMLNTLR 76

RESULT 10
Q9FGY3 PRELIMINARY; PRT; 307 AA.
ID Q9FGY3
AC Q9FGY3;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYB-RELATED TRANSCRIPTION FACTOR.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones.";
RL DNA Res. 7:31-63(2000).
DR EMBL; AB023033; BAB10776.1; -.
DR HSSP; P01103; IPOW.

RA Buchler M.K., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,
RA Dunn P., Etyu P., Feildlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmid A.D., Haas B., Hansen N.F., Hughes B., Hutzar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maltl R., Marzibelli A.,
RA Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakanu H., Sailer J.S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
RT "Sequence and analysis of chromosome 1 of the plant *Arabidopsis*
RT *thaliana*.";
RL Nature 408:816-820(2000).
DR EMBL: AC016447; AAC52612.1; -.
DR HSSP: P06876; IMBG.
DR InterPro: IPR001005; MYB_DNA_bind.
DR Pfam: PF00249; myb_DNA-binding; 2.
DR SMART: SM00395; SANT; 2.
DR PROSITE: PSS0090; MYB_3; 2.
SQ SEQUENCE 286 AA; 35239 MW; C6765A6B744CC717 CRC64;
